



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/891,119
Source: OPE
Date Processed by STIC: 3/25/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202**
- 3. Hand Carry directly to:**
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202**

Raw Sequence Listing Error Summary

018

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/891,119
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



OIPE

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/891,119

DATE: 03/25/2003

TIME: 12:47:11

Errors on p. 4.

Input Set : A:\24577-CY-B.ST25.txt

Output Set: N:\CRF4\03252003\I891119.raw

3 <110> APPLICANT: Maddon, Paul J.
 5 <120> TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
 7 <130> FILE REFERENCE: 24577-CY-B
 9 <140> CURRENT APPLICATION NUMBER: 09/891,119
 10 <141> CURRENT FILING DATE: 2001-06-25
 12 <160> NUMBER OF SEQ ID NOS: 22
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1273
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Human
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 23 <222> LOCATION: (76)..(1257)
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38	1 5 10	
40	gtg ctg caa ctg gcg ctc ctc cca gca gcc act cag gga aag aaa gtg	159
41	Val Leu Gln Leu Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val	
42	15 20 25	
44	gtg ctg ggc aaa aaa ggg gat aca gtg gaa ctg acc tgt aca gct tcc	207
45	Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser	
46	30 35 40	
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50	45 50 55 60	
52	att ctg gga aat cag ggc tcc tcc tta act aaa ggt cca tcc aag ctg	303
53	Ile Leu Gly Asn Gln Gly Ser Ser Leu Thr Lys Gly Pro Ser Lys Leu	
54	65 70 75	
56	aat gat cgc gct gac tca aga aga agc ctt tgg gac caa gga aac ttc	351
57	Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe	
58	80 85 90	
60	ccc ctg atc atc agg aat ctt aag ata gaa gac tca gat act tac atc	399
61	Pro Leu Ile Ile Arg Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile	
62	95 100 105	
64	tgt gaa gtg gag gac cag aag gag gag gtg caa ttg cta gtg ttc gga	447

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Input Set : A:\24577-CY-B.ST25.txt

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69	Leu	Thr	Ala	Asn	Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	
70	125					130					135				140		
72	ctg	acc	ttg	gag	agc	ccc	cct	ggt	agt	agc	ccc	tca	gtg	caa	tgt	agg	543
73	Leu	Thr	Leu	Glu	Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	
74					145					150					155		
76	agt	cca	agg	ggt	aaa	aac	ata	cag	ggg	ggg	aag	acc	ctc	tcc	gtg	tct	591
77	Ser	Pro	Arg	Gly	Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	
78				160					165					170			
80	cag	ctg	gag	ctc	cag	gat	agt	ggc	acc	tgg	aca	tgc	act	gtc	ttg	cag	639
81	Gln	Leu	Glu	Leu	Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	
82			175					180					185				
84	aac	cag	aag	aag	gtg	gag	ttc	aaa	ata	gac	atc	gtg	gtg	cta	gct	ttc	687
85	Asn	Gln	Lys	Lys	Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	
86		190					195				200						
88	cag	aag	gcc	tcc	agc	ata	gtc	tat	aag	aaa	gag	ggg	gaa	cag	gtg	gac	735
89	Gln	Lys	Ala	Ser	Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Asp	
90	205					210					215				220		
92	ttc	tcc	ttc	cca	ctc	gcc	ttt	aca	gtt	gaa	aag	ctg	acg	ggc	agt	ggc	783
93	Phe	Ser	Phe	Pro	Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	
94				225					230					235			
96	gag	ctg	tgg	tgg	cag	gcg	gag	agg	gct	tcc	tcc	tcc	aag	tct	tgg	atc	831
97	Glu	Leu	Trp	Trp	Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	
98				240					245					250			
100	acc	ttt	gac	ctg	aag	aac	aag	gaa	gtg	tct	gta	aaa	cgg	gtt	acc	cag	879
101	Thr	Phe	Asp	Leu	Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	
102			255					260					265				
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105	Asp	Pro	Lys	Leu	Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	
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108	ccc	cag	gcc	ttg	cct	cag	tat	gct	ggc	tct	gga	aac	ctc	acc	ctg	gcc	975
109	Pro	Gln	Ala	Leu	Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	
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112	ctt	gaa	gcg	aaa	aca	gga	aag	ttg	cat	cag	gaa	gtg	aac	ctg	gtg	gtg	1023
113	Leu	Glu	Ala	Lys	Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	
114				305					310				315				
116	atg	aga	gcc	act	cag	ctc	cag	aaa	aat	ttg	acc	tgt	gag	gtg	tgg	gga	1071
117	Met	Arg	Ala	Thr	Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	
118				320					325				330				
120	ccc	acc	tcc	cct	aag	ctg	atg	ctg	agc	ttg	aaa	ctg	gag	aac	aag	gag	1119
121	Pro	Thr	Ser	Pro	Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	
122			335					340					345				
124	gca	aag	gtc	tcg	aag	cgg	gag	aag	gcg	gtg	tgg	gtg	ctg	aac	cct	gag	1167
125	Ala	Lys	Val	Ser	Lys	Arg	Glu	Lys	Ala	Val	Trp	Val	Leu	Asn	Pro	Glu	
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128	gcg	ggg	atg	tgg	cag	tgt	ctg	ctg	agt	gac	tcg	gga	cag	gtc	ctg	ctg	1215
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153          20          25          30
156 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
157          35          40          45
160 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
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164 Gln Gly Ser Ser Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
165 65          70          75          80
168 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
169          85          90          95
172 Arg Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
173          100         105         110
176 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
177          115         120         125
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181          130         135         140
184 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
185 145         150         155         160
188 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
189          165         170         175
192 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
193          180         185         190
196 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
197          195         200         205
200 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Asp Phe Ser Phe Pro
201          210         215         220
204 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
205 225         230         235         240
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213          260         265         270
216 Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
217          275         280         285
220 Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
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Output Set: N:\CRF4\03252003\I891119.raw

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 228 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
 229 325 330 335
 232 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
 233 340 345 350
 236 Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
 237 355 360 365
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 279 <212> TYPE: DNA
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 301 caagcccaga gccctgccat ttctgtgggc tcaggteccct actgtcagc cccttctcc 60

invalid response, see error summary sheet
item 10

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

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Input Set : A:\24577-CY-B.ST25.txt

Output Set: N:\CRF4\03252003\I891119.raw

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311 ctgaatgatc gcgctgactc aagaagaagc ctttgggacc aaggaaactt cccctgatc 360
313 atcaagaatc ttaagataga agactcagat acttacatct gtgaagtgga ggaccagaag 420
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325 ggggaacagg tggagttctc cttccactc gcctttacag ttgaaaagct gacgggcagt 780
327 ggcgagctgt ggtggcaggc ggagagggtt tctcctcca agtcttgat cacctttgac 840
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377 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
378 35 40 45
381 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
382 50 55 60
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386 65 70 75 80
389 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
390 85 90 95
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394 100 105 110
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/891,119

DATE: 03/25/2003

TIME: 12:47:12

Input Set : A:\24577-CY-B.ST25.txt

Output Set: N:\CRF4\03252003\I891119.raw

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